GENE PROFILING OF SINGLE OR MULTIPLE CELLS

Abstract

An mRNA is amplified by *(a)* binding a first primer to a target mRNA, the first primer comprising, in the 5' to 3' direction, a first known segment and an oligo T segment; *(b)* transcribing a cDNA from said target mRNA by elongation of said first primer with reverse transcriptase; and then *(c)* linking a second known segment to the 3' terminus of said cDNA. In a preferred embodiment the step of transcribing a cDNA from said target mRNA is carried out so that at least one additional C residue is produced on the 3' terminus of said cDNA, and the said step of linking a second known segment to the 3' terminus of said cDNA is carried out by: *(i)* binding a second bridge primer to said cDNA, said second primer comprising, in the 5' to 3' direction, a second known segment and at least one G residue, said second primer having an inactivated G residue on the 3' terminus thereof; and then *(ii)* further transcribing said cDNA from second bridge primer by elongation of said at least one additional C residue with reverse transcriptase so that a cDNA is produced having said first known segment on the 5' terminus thereof and said second known segment on the 3' terminus thereof. The method can be used to amplify a plurality of mRNAs together, even though a small sample of mRNAs is available suchas obtained from a single cell or multiple cells obtained by laser capture microdissection from tissue or organs, and the product of the amplification then used for gene family analysis or microarray expression analysis.